Title: Perfect score: Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

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Propionibacterium
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Mycobacterium tube
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Triticum aestivum
Triticum aestivum
Psudomonas sp ABC
Psudomonas sp ABC
  Artificial DNA seq
plasmid pBS149 2X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pKS133 2X ELVISLIVES complementary repeat DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product "ELVISLIVES protein"
44.74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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AAF60762
AAC04565
AAC04565
AAH52046
AAH52046
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AA199682
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AAI99683
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AA166075
                                                                            AAD29230
ABK10712
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ABK10710
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AAS18438
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AAS59803
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AAQ89779
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Plasmid pkS133 2X
Plasmids pkS133 2X
Plasmid pkS133 2X
Plasmid pkS133 DNA
Plasmid pkS133 DNA
PBS68 plasmid used
PBS68 plasmid used
Artificial DNA seq
                                                                                                 (without alignments)
1275.028 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                            | Side | 
                                                                                                                                                              l cggccggagctggtcatctc.....gagatgaccagctccggccg 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                   November 19, 2002, 03:54:43; Search time 272 Seconds
            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                          2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          - nucleic search, using sw model
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AAD32908
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length: 2000000000
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/product "ELVISLIVES protein"

WO200216565-A2

AAD32909 AAD32909 ABK10711

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                                                                                                                                                                                                                                                                                                    The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, eg. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce an unimal contains to produce is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133 This sequence is used in the exemplification of the invention for the suppression of Fad2 in soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pKS133;
                                                                                                                                                                                             delta-9 fatty acid desaturase polypeptides and polynucleotides, ful in creating transgenic plants having altered levels of mono-, and unsaturated fatty acids and in increasing the unsaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGAGCTGGTCATCTCGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 154; DB 24; Length 154; 100.0%; Pred. No. 6.5e-29; ive 0; Mismatches 0; Indels 0
                                                                                                                      Yadav NS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;
                                                                                                                    Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ACTCGACGATGAGGGAGATGACCAGCTCCGGCCG 154
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                                                                                                                                                                                                                                                                           Example 9; Page 43; 77pp; English.
                                                                                                                      Hitz WD,
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                           22-AUG-2001; 2001WO-US26246.
                                                        22-AUG-2000; 2000US-226996P
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ID AAD32908 standard; DNA; 154
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                                                                                                                                                                                                                                            levels in cellular lipids
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                                                                                                                                                WPI; 2002-269353/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                P-PSDB; AAE20554
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Matches 154;
                                                                                                                    Booth JR,
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The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thuse altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is 1X ELVISILVES complementary repeat region DNA found in plasmid pKS133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           creating transgenic plants having altered levels of mono-, unsaturated fatty acids and in increasing the unsaturation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hitz WD, Kinney AJ, Yadav NS;
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                                                                                                                      /product= "ELVISLIVES protein" complement (82..111)
                                                                                                                                                                                                              /product "ELVISLIVES protein" complement (119..148)
                                "ELVISLIVES protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2001; 2001WO-US26246.
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P-PSDB; AAE20554.
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Matches 154;
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CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120

BP

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61 CATCGTCGACTCGCCGCCGCCGACTCGACGATGACGAGATGACCAGCTCCGGCCGCCG 120
                                                                                                                                                                    121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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ID AAD29231 standard; DNA; 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stecca KL;
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                                                                                                                                                                                                                         Recombinant construct; gene expression; plasmid pKS133; ds.
                                                                                                                                                                    Plasmids pKS133 2X ELVISLIVES complementary repeat DNA
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; Pred. No. 6.5e+29;
0; Mismatches 0;
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/product= "ELVISLIVES protein"
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complement (119..148)
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ilarity 100.0%;
Conservative 0
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AAD29231 standard; DNA; 154
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reducing gene expression
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/*tag=
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                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                            07-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The sequences from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
                                                                                        ds.
                                                                                        Recombinant construct; gene expression; plasmid pKS133;
                                                          Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
                                                                                                                                                                                                                                                                                      protein"
                                                                                                                                                                                                                                                                                                                                    /product- "ELVISLIVES protein"
                                                                                                                                                                                                                                            *ELVISLIVES protein
                                                                                                                                                                                              *ELVISLIVES protein
                                                                                                                                                                                                                                                                                      /product= "ELVISLIVES complement (119..148)
                                                                                                                                                                                                                                                          complement (82.111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 45; Page 37; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001; 2001WO-US19962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-2000; 2000US-213961P.
                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  WO200200904-A2.
                                                                                                                      Unidentified
                             07-MAY-2002
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Indels

Local Similarity

Matches 154;

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1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transforming a host cell with a chimeric gene and growing the transformed
it. The present sequence is 2X ELVISLIVES complementary repeat region DNA found in plasmid pKS133 used in the exemplification of the invention.
                                                                                                                                                                                                                               CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
                                                                                                                       Gaps
                                                                                                                                                         9
                                                                                                                                                                                                                                            154 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                         a plastidic phosphoglucomutase protein in a host cell comprises
                                                                                                                       ö
                                                                                       Length 154;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
                                                   Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;
                                                                                    100.0%; Score 154; DB 24;
100.0%; Pred. No. 6.5e-29;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                                                                                                   ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                                                                                                                                                                                                                                                                  ACTCGACGATGAGGGAGATGACCAGCTCGGGCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carlson TJ, Ilag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; SEQ ID No 17; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-2001; 2001EP-0306143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2000; 2000US-218712P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                        Best Local Similarity 100.
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Butler KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-156692/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pKS133 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1174510-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK10072;
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           levels
                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                   121
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The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of transgenic plant, by transforming a plant from the transformed plant cell. Solutions are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least SI nucleotides, measuring the level of the polypeptide in the polynucleotide, and comparing the level of the polypeptide in the plant cell containing the isolated polynucleotide with the isolated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protech in a host cell comprises transformed transformed
                                                                                                                                                                                                             ó
cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents plasmid DNA used in the methods of the invention.

Note: This sequence is not represented in the printed specification but
                                                                                             based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                       4863 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGGCCGGAGCTGGTCTCGCCT 4922
                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                 1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGGCGGCCGGAGCTGGTCATCTCGCT
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                               61 CATCGTCGAGTCGCCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCC 112
                                                                                                                                                                       Length 4974;
                                                                                                                                   Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 1 other;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
                                                                                                                                                                       72.7%; Score 112; DB 24;
100.0%; Pred. No. 1.3e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carlson TJ, Ilag LL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2002 (first entry)
                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 112; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-156692/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pKS133 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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ABK10072/c
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New delta-9 fatty acid desaturase polypeptides and polynucleotides,
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                                                                                                                                                                                                                        Query Match
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Matches
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cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents plasmid DNA used in the methods of the invention.

Note: This sequence is not represented in the printed specification but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-
                                                                                                                                                               43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
                                                                                                                                                                                                                                                                                                                                                                         Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly- and unsaturated fatty acids and in increasing the unsaturation
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                   pBS68 plasmid used for diverged delta-9 desaturase suppression.
                                                                                                                                                                                                          4914 GACCAGCTCCGGCCGCCGACATCGACGAGAGCGAGATGACCAGCTCCGGCCG 4863
                                                                                                     72.7%; Score 112; DB 24; Length 4974; ilarity 100.0%; Pred. No. 1.3e-18; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                103 GACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
                                                                               Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yadav NS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag- b
/label- Kit3_terminator
complement (880..1920)
/*tag- b
/note- "Hygromycin selection region"
3260..5348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinney AJ,
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/label= Kit3_promoter
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                                                                                                                                                                                                                                                                                                                             (first entry)
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levels in cellular lipids
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                                                                                                                Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200216565-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                       AAD32909;
                                                                                                      Query Match
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Limiting, to isolate CDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the same or other plant at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is plasmid pBS68 which is used for the suppression of diverged delta-9 desaturase in high stearate phenotypes. This sequence is used in the exemplification of the invention.

Where: The sequence data for this sequence (AAD32909) corresponding to position 1501 to 6611 is not represented in the printed specification but is based on the sequence information supplied by the European patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82.8; DB 24; Length 6611;
Pred. No. 1.7e-11;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 661, BP; 1831 A; 1472 C; 1453 G; 1854 T; 1 other;
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/note= "Hygromycin selection region"
3260..5348
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/label= Kit3_terminator
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/label= Kit3_promoter
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523..725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD32909/c
ID AAD32909 standard; DNA; 6611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 53.8%;
l Similarity 97.7%;
84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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us-09-887-194a-13.rng

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The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, eg. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is plasmid pBSG8 which is used for the suppression of diverged delta-9 community and as used to the suppression of diverged in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention.

Note: The sequence data for this sequence (AAD32909) corresponding to position 1501 to 6611 is not represented in the printed specification but is based on the sequence information supplied by the European patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 AGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
useful in creating transgenic plants having altered levels of mono-, poly- and unsaturated fatty acids and in increasing the unsaturation levels in cellular lipids - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82.8; DB 24; Length 6611;
Pred. No. 1.7e-11;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note" "No start or stop codon shown"
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/note= "No start or stop codon shown"
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/product* "ELVISLIVES peptide"
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                                                                     Example 9; Page 76-77; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5373 ATGAGCGAGATGACCAGCTCCGGCCG 5348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 ATGAGCGAGATGACCAGCTCCGGCCG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 53.8%;
1 Similarity 97.7%;
84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK10711;
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The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polyucleotide of the invention and regenerating a plant from the transformed plant cell.

The invention and regenerating a plant from the transformed plant cell.

Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide baying the level of phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a level of east 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide in the plant cell containing the level of the polypeptide in a plant cell containing the solated polynucleotide. A method for altering the level of expression of a plant cell wider conditions that are suitable for expression of the chimeric cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plastidic phosphoglucomutase; transgenic; plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 3.8e-11; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7..36
/*tag-
/product- "ELVISLIVES peptide"
/partial
                                                                                        Carlson TJ, Ilag LL;
                                                   (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                      Example 9; Page 19; 27pp; English.
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               17-JUL-2000; 2000US-218712P.
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ID ABK10711 standard; DNA; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CATCGTCGAGTCGGCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CATCGTCGAGTCGCCGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 81; Conservative
                                                                                      Allen SM, Butler KH,
                                                                                                                      WPI; 2002-156692/21.
                                                                                                                                          P-PSDB; AAU77109
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%XGGGGGGGGGGGGGCX8XFFFFFFXXBXXBXXBXXBXXBXXBX
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The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polyuclocitide of the invention and regenerating a plant from the transformed plant cell. Polynuclectide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynuclectide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nuclectides, measuring the level of the polypeptide in the plant cell containing the polypuclectide, and comparing the level of the polypeptide in a plant cell containing the lavel of the polypeptide in a plant cell that does not contain the isolated polypuclectide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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0
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                                /*tag= b/product= ELVISLIVES peptide"
/partial
/note= "No start or stop codon shown"
 'note= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                               Carlson TJ, Ilag LL;
                                                                                                                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Page 19; 27pp; English.
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                                                                                                                                                                                       17-JUL-2001; 2001EP-0306143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81; Conservative
                                                                                                                                                                                                                                                                                                 Allen SM, Butler KH,
                                                                                                                                                                                                                                                                                                                              WPI; 2002-156692/21.
P-PSDB; AAU77109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                    EP1174510-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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                  CDS
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construct comprises a produces on RNA having homology to at least one when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous of genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 2X ELVISLIVES complementary region from the present sequence is 2X ELVISLIVES complementary region from GASI and GASI. The region is functionally attached to a late-soybean entire region is then cloned into BamHI site of PKSI36, which contains a continuation of the BamHI site of PKSI36, which contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2X ELVISLIVES complementary region controlled by a soybean Kti promoter and terminator region used in the exemplification of the invention.
                                                    Recombinant construct; gene expression; late-soybean-embryo promoter;
LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GCGGCCGCCGACTCGACGATGACGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new recombinant construct. The
                                                                                                                                                                                                                                                                                                                                                                     Stecca KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.3e-11;
; Mismatches 0; Indels
              Plasmid pBS149 2X ELVISLIVES complementary region DNA
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                                                                                                                                                                                                                                                                                                                                                                     Lowe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81; DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 4.3
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Glassman KF, Gordon-Kamm WJ, Kinney AJ,
                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Page 72; 77pp; English.
                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 CGAGATGACCAGCTCCGGCCG 154
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                                                                                                                                                                                                                             22-JUN-2001; 2001WO-US19962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reducing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                           NPI; 2002-139927/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                 WO200200904-A2.
                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-2002
                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                         Nichols SE;
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AAD29247/C
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P-PSDB: AAE20554
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                                                              Unidentified
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AAD32907/c
ID AAD3290
XX
                                                                                                                                          SDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
  g
                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the cecombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from 15.714 present sequence is 2X ELVISLIVES complementary region from passive the region is functionally attached to a late-soybean-embry promoter (LEA) and a phaseolin 3′ terminator region. This entire region is then cloned into Bamil site of pKS136, which contains a 2X ELVISLIVES complementary region controlled by a soybean Kti promoter and terminator region used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                          New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant construct; gene expression; late-soybean-embryo promoter;
LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
                                                                                                                                                                                                                                Stecca KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.6%; Score 81; DB 24; Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; . Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 other;
Plasmid pBS149 2X ELVISLIVES complementary region DNA
                                                                                                                                                                                                                                 Lowe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%; Pred. No. 4.3
Matches 81; Conservative 0; Mismatches
                                                                                                                                                                                                                                Glassman KF, Gordon-Kamm WJ, Kinney AJ,
                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO E I.
(PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                            Example 10; Page 72; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    903 CATCGTCGAGTCGCGGCCGC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                          22-JUN-2001; 2001WO-US19962,
                                                                                                                                                                 23-JUN-2000; 2000US-213961P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCGTCGAGTCGGCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD32907 standard; DNA; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                     reducing gene expression
                                                                                                                                                                                                                                                                  WPI; 2002-139927/18.
                                                                                      WO200200904 - A2
                                                                Unidentified.
                                                                                                                 03-JAN-2002.
                                                                                                                                                                                                                                            Nichols SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD32907;
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The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or raterilating, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normally found thus altering the level of monor, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RPLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence antibodies specific for the peptides and proteins. The present sequence is IN ELVISLIVES complementary repeat region DNA found in plasmids pKS106 and pKS214. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly- and unsaturated fatty acids and in increasing the unsaturation
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Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pKS124; plasmid pKS106; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 51.9%; Score 80; DB 24; Length 80; Best Local Similarity 100.0%; Pred. No. 6.7e-11; Matches 80; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hitz WD, Kinney AJ, Yadav NS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag* b
/product* "ELVISLIVES protein"
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/product= "ELVISLIVES protein"
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                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (45..74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 43; 77pp; English.
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us-09-887-194a-13.rng

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Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
                                                                                                                                                                                                                                                                                                              Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
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Nichols SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
                                                                                                       AAD29230 standard; DNA; 80 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                 RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono., poly- and unsaturated fatty acids and in increasing the unsaturation
                                                                                                                                                                                                          Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil; transgenic plant; gene mapping; immunisation; plasmid pKS124; plasmid pKS106; gene; ds.
                                                                                                                                           Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinney AJ, Yadav NS;
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                                                                     (first entry)
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P-PSDB; AAE20554.
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                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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AAD32907;
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PONT DE NEMOURS & CO E I.

2000US-213961P.

/product= "ELVISLIVES protein" /product= "ELVISLIVES protein" complement (45.74)

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Location/Qualifiers

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New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 80; DB 24; Length 80; 100.0%; Pred. No. 6.7e-11;
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                                                                                                                              reducing gene expression
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SUMMARIES

ì	Description	288-7 Sequence 7, Appli	Sequence 7,	Sequence 2.	Sequence 1,	Sequence 1.		Sequence 1, A	-1 Sequence 1,	Sequence 6,	Sequence 6,	Sequence 40,	Sequence 40,	Sequence 21,	21 Sequence 21,	535		l Sequence 1	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 49,	Sequence 49,	Sequence 1, 7	1 Sequence 1,	Sequence 4,	-4 Sequence 4,	
	ID	US-09-434-288-7	US-09-434-288-7	US-09-103-840A-2	US-09-103-840A-1	US-09-103-840A-	US-09-103-840A-2	US-07-841-651-1	US-07-841-651	US-09-032-372-6	US-09-032-372-6	US-09-105-537-40	US-09-105-537-40	US-09-320-878-21	US-09-320-878-	5352575-8	5352575-8	US-07-642-	US-07-642-734C-	US-08-439-009A-1	US-08-439-009A-	US-08-984-709A-49	US-08-984-709A-49	US-08-809-740A-1	US-08-809-740A-	US-08-809-740A-4	US-08-809-740A	444 744 44
	Match Length DB	1681 4	1681 4	4403765 4	4411529 4	4411529 4	4403765 4	2238 1	2238 1	2119 3	2119 3	2787 4	2787 4	5970 3	5970 3	1734 6	1734 6	11219 1	11219 1	11219 3	11219 3	7898 4	7898 4	3252 2	3252 2	3252 2	3252 2	
% Query	Match	22.6	22.6	22.1	22.1	22.1	21.3	21,0	21.0	20.8	20.8	20.0	20.0	20.0	20.0	19.9	19.9	19.7	19.7	19.7	19.7	19.6	19.6	19.4	19.4	19.4	19.4	1
	Score	34.8	34.8	34	34	34	32.8	32.4	32.4	32	32	30.8	30.8	30.8	30.8	30.6	30.6	30.4	30.4	30.4	30.4	30.2	30.2	29.8	29.8	29.8	29.8	
Result	No.	7	7 0	3	4	O 5	9	7	ထ	6	c 10	11	c 12	13	c 14	15	c 16	17	c 18	19	c 20	21	c 22	23	c 34	25	c 26	,

Sequence 3, Appli Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli	ENZYMES AND RECOMBINANT DNA	Length 1681; ; Indels 0; Gaps 0; GGAGCTGGTCATCTGGT 60	ENZYMES AND RECOMBINANT DNA
6822 4 US-09-426-998-3 7741 4 US-09-426-998-4 7741 4 US-09-426-998-4 1790 4 US-09-133-962A-7 2335 4 US-09-387-574-9 2335 4 US-09-387-574-9 2335 4 US-09-68-096-9 2335 4 US-09-68-096-9 4848 4 US-08-955-957A-1 4848 4 US-08-955-957A-1 4848 4 US-08-955-957A-4 4848 4 US-08-955-957A-4 4848 4 US-08-955-957A-4 4848 4 US-08-955-957A-6 4848 4 US-08-955-957A-6 4848 4 US-08-955-957A-6 1296 1 US-07-816-283-9	HASE EFOR 4,286	22.6%; Score 34.8; DB 4; 55.9%; Pred. No. 1.4; tive 0; Mismatches 52 ATCTCGCTCATCGTCGAGTCGCGGCC GGCGCTCATCGTCGGGGCGGCGGCGGGCGGGGGGGGGG	THASE REFOR 34,286
C 28 29.4 19.1 28.8 18.7 C 3.6 29.4 19.1 28.8 18.7 C 3.6 28.8 18.7 C 4.0 28.8 18.7 C 4.1 28.8 18.8 C 4.1 28.8 18.8 C 4.1 28.8	ALIU US-09-434-288-7 Sequence 7, Application US/09434288 Patent No. 6303767 GENERAL INFORMATION: APPLICANT: Betlach C., Melanie APPLICANT: Betlach C., Melanie TITLE OF INVENTION: POLYKETIDE SYNT: TITLE OF INVENTION: POLYKETIDE SYNT: FILE OF INVENTION: CONSTRUCTS THERE FILE REFERENCE: 30062-20030.00 CURRENT FILING DATE: 1999-11-05 PRIOR PILING DATE: 1999-11-05 PRIOR FILING DATE: 1998-11-05 SOFTWARE: PATENTIN NUMBER: 60/107,09 PRIOR FILING DATE: 1998-11-05 TURBER OF SEQ ID NOS: 12 SOFTWARE: PATENTIN VET. 2.1 SEQ ID NO 7 LENGTH: 1681 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA	Query Match Best Local Similarity 55. Matches 66; Conservative Qy 1 CGGCGGAGCTGGTCATCT Db 424 CTGGCGCGCTGCTCAGCG Qy 61 CATCGTCGAGTGGGCGC Oy 61 CATCGTCGAGTGGGCGC Db 484 CGCCGCAGGCCGCCCCC	RESULT 2 US-09-14-288-7/C Sequence 7, Application US/09434288 Patent No. 6303767 GENERAL INFORMATION: APPLICANT: Betlach C., Melanie: APPLICANT: Betlach C., Melanie: TITLE OF INVENTION: POLYKETIDE SYN TITLE OF INVENTION: CONSTRUCTS THE FILE REFERENCE: 3062-20030.00 CURRENT FILING DATE: 1999-11-05 PRIOR FILING DATE: 1998-11-05 NUMBER OF SEQ ID NOS: 12

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Patentin Ver. 2.1
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve.
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                                                        LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-103-840A-1/c
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US-09-103-840A-2
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                                       SEQ ID NO 1
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CTHER INFORMATION: CDC 1551
CTHER INFORMATION: "n" bases at various positions throughout the sequence
CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: WHITE, Owen R.
APPLICANT: WITER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICANTION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                               APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WITER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TOBERCHICASIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                    37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACGACGATGAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 GCGCCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCCCCCCACTCGACGATGAG 96
                                                                                                                                                                                                                                                                                                  97 CGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 4251831 CGGGGTGTCCAGCTTCGGCTGGGGGCGCCAACGCGC 4251794
                                                                                                                                      Score 34.8; DB 4;
Pred. No. 1.4;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                        ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-7
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                      Query Match 22.6%;
Best Local Similarity 55.9%;
Matches 66; Conservative
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Best Local Similarity 59.2
Matches 58; Conservative
  PatentIn Ver.
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                                     LENGTH: 1681
SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                          Matches
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Db 4259635 GCGGTTGAGATGATCACCACGCCACCGACTGCCGCGCATACGCCGGCTACGCCCTGGC 4259576
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE OF INVENTION: TUBERCULOSIS
FILE REPERRACE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFFWARRE: PATENTIN VET: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, OLD NO.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                  21 GCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCGGCCG 80
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                                                                                                                                 DB 4; Length 4411529;
                                                                                                                                                                                 40; Indels
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                                                                                                                              Score 34; DB 4
Pred. No. 2.3;
                                                                                                                                                                            0; Mismatches
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COTHER INFORMATION: H37Rv
US-09-103-840A-1
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                              22.1%;
59.2%;
                                                                                                                           Query Match
Best Local Similarity 59.24
Matches 58; Conservative
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Best Local Similarity 59.29
Matches 58; Conservative
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Length 2238;

Score 32.4; DB 1; Length 2 Pred. No. 5.1; 0; Mismatches 31; Indels

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70 GTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGA 129
                                                                                                                                                                                     130 TGAGCGAGATGACCAGCTCCGG 151
                                                                                                                                                                                                                           786 TGACTCCTATCATCTGCTCCGG 807
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                     21.0%;
62.2%;
                                                             Conservative
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                     Query Match
Best Local Similarity
Matches 51; Conserva
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Best Local Similarity
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ORGANISM: Or
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US-07-841-651-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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APPLICANT: Wright, Ernest M
TITLE OF INVENTION: Cloning and Functional Expression of a
TITLE OF INVENTION: Manmalian Na+/Nucleoside Cotransporter: A Member of the
TITLE OF INVENTION: SGLT Family
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                Db 4251794 GCGCGTTGGCGCCGCCGAAGCCGAAGCTGGACACCCCGGCCAGCGCGTAGCCGCCGTATC 4251853
                                                                                                 FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                            21 GCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCG 80
                                                                                                                                                                                                                           DB 4; Length 4403765;
                                                                                                                                                                                                                         Query Match 21.3%; Score 32.8; DB 4; Length 4 Best Local Similarity 59.2%; Pred. No. 4.3; Matches 58; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Db 4251854 GCGGCCAGTCGTGGCGTGGTGATCTTTCAACCGC 4251891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,651
FILING DATE: 19920224
                                                                                                                                                                                                                                                                                                                                                                                        81 CCGACTCGACGATGACCGAGATGACCAGCTCCGGCCGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon 6 Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                              ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19920224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 9772
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07841651
Patent No. 5410031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (818) 795-4000 TELEFAX: (818) 795-6521 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2238 base pairs
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 91101
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; LOCATION:
US-07-841-651-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-841-651-1
                                                             TYPE: DNA
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| Sequence 1, Application US/07841651
| Sequence 1, Application US/07841651
| Patent No. 5410031
| GENERAL INFORMATION:
| APPLICANT: Wright. Exnest M
| APPLICANT: Wright. Exnest M
| TITLE OF INVENTION: Cloning and Functional Expression of a
| TITLE OF INVENTION: SGLT Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: 0S/07/841,651
FILING DATE: 19920224
                                                                                                                                                                                                                                                          ADDRESSEE: Sheldon 6 Mak
STREET: 225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32.4; DB
Pred. No. 5.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,853
REGISTRATION NUMBER: 31,853
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1906-4000
TELECAMATION 180 796-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.0%;
62.2%;
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                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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67 CGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Indels
                                                                                                APPLICANT: COTLEY, Neil C.
APPLICANT: COTLEY, Neil C.
APPLICANT: Googler, Karl J.
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
TILLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ResEED for Windows Version 2.0 SOFTWARE: ResEED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith CLASSIFICATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY APPLICATION APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 3;
Pred. No. 6.4;
0; Mismatches
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; BEREAL INFORMATION:
; APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 CGATGAGCGAGATGACCAGCTCCG 150
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            Sequence 6, Application US/09032372 Patent No. 6008337 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                           APPLICANT: Bandman, Olga APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                            2IP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERAING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 20.8%;
Best Local Similarity 51.4%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-09-032-372-6/c
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US-09-105-537-40
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US-09-032-372-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGGCCGGAGCTGGTCATCTCGCTCATC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%; Score 32; DB 3; Length 2119; 51.4%; Pred. No. 6.4;
                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preetl
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPREATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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ATORNEY/AERT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                   Sequence 6, Application US/09032372 Patent No. 6008337
                                                                                                                                                                               Bandman, Olga
Hillman, Jennifer L.
747 AGCCGGGTCCTCGGACACCGTC 726
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LENGTH: 2119 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
COUNTR: USA
ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 78191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bandma
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                                                                                                  US-09-032-372-6
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RESULT 10

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2815 CGCTCTTACTCGTCTCCGGACCGGCAGCGGGAAGACGCGGAGCTGCTGCGGTCGCTCC 2874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: TANG, Li
TILLE REPERBNE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER PLING DATE: 1998-09-22
EARLIER PLING DATE: 1998-05-28
EARLIER PLING DATE: 1998-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.0%; Score 30.8; DB 3; 18est Local Similarity 57.1%; Pred. No. 13; Matches 56; Conservative 0; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 GCCGACTCGACGATGACCGAGATGACCAGCTCCGGCCG 154
                     EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: GO 108,846,247
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER PILING DATE: 1999-03-08
EARLIER PILING DATE: 1999-03-08
EARLIER FILING DATE: 1998-03-28
EARLIER FILING DATE: 1998-05-28
WUMBER OF SEQ ID NOST: 34
SOFTWARE: PATENTIN VET: 2.0
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  FILING DATE: 1999-05-27
APPLICATION NUMBER: CIP OF 09/141,908
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces venezuelae US-09-320-878-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21
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ilarity 57.1%;
Conservative
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Matches 56; Conserv
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US-09-320-878-21/C
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SEQ ID NO 21
LENGTH: 5970
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5970
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 2787;
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US-09-105-537-40/c
; Sequence 40, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sharman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Liu, H.
; TILE OF INVENTION: DNA encoding methymycin and pikromycin; FILE REPERENCE: 600.438US1
; CURRENT APPLICATION UNBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 40
LENGTH: 2787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 GCCGCTGGCCGCCGAGCGGGAGACCCCCGTCTGGTCG 174
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                                                                                                                                                                                                                                                                                                           Score 30.8; DE
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.0%; Score 30.8; D
Best Local Similarity 57.1%; Pred. No. 12;
Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09320878A Patent No. 6117659
GENERAL INFORMATION:
                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Streptomyces venezuelae US-09-105-537-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
                                                                                                                                                                                                                                                                                                           20.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                         56; Conservative
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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LENGTH: 2787
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US-09-320-878-21
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                                                                                                                                                                                                                                                                                                                                                           Matches
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TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/513,282
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: 100,817
FILING DATE: 10-APR-1986
APPLICATION NUMBER: 86,260
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 86,260
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 801,799
FILING DATE: 26-AWR-1986
APPLICATION NUMBER: 81,799
FILING DATE: 26-WAR-1986
1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGCCGGAGCTGGTCATCTCCCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 CTCATCGTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.6; DB 6; Length 17
Pred. No. 14;
0; Mismatches 64; Indels
                                                                                             2852 CTTCCCGCTGCCGGTCCGGAGACGAGGAGGG 2815
                                                                    61 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: November 19, 2002, 07:40:47 Job time: 8178 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.9%;
Best Local Similarity 51.9%;
Matches 69; Conservative
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                                                                                                                                                                                                       Patent No. 5352575
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sequence 93, Appl Sequence 98, Appl Sequence 171, Appl Sequence 78, Appl Sequence 78, Appl Sequence 68, Appl Sequence 68, Appl Sequence 4679, Appl Sequence 4679, Appl Sequence 391, Appl Sequence 1149, Appl Sequence 1149, Appl Sequence 2203, Appl Sequence 2203, Appl Sequence 2203, Appl Sequence 2279, Appl Sequence 2279, Appl Sequence 2279, Appl Sequence 390, Appl Sequence 390, Appl Sequence 390, Appl Sequence 379, Appl Sequence 1779, Appl Sequence 1779, Appl Sequence 2779, Appl Sequence 1779, Appl

Perfect score: Sequence: Scoring table:

Searched:

Database

nucleic

Run on:

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1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.7%; Score 112; DB 9; Length 4974; Best Local Similarity 100.0%; Pred. No. 5.7e-22; Matches 112; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09906209
Fatent No. US20020165385A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: Carlson, Tom
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB145.1 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR PLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
SOTTAMER: Microsoft Office 97
LENGTH: 4974
               US-09-822-8308-93

US-09-822-8308-93

US-09-822-8308-93

US-09-764-853-98

US-09-764-853-98

US-09-712-363-78

US-09-712-363-78

US-09-712-363-68

US-09-712-363-68
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US-09-133-590-4679
US-09-813-790-391
US-09-867-550-1149
US-09-867-550-1149
US-09-880-107-2203
US-09-880-107-2203
US-09-880-107-2203
US-09-880-107-2279
US-09-880-107-2279
US-09-880-107-2279
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US-09-867-550-87
US-09-867-550-87
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  1536 . 2280 . 2280 . 427 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 2280 . 228
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US-09-906-209-17
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  NAME/KEY: unsure
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                                                                                                      TYPE: DNA
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Sequence 100, Appl
Sequence 100, Appl
Sequence 20, Appl
Sequence 7752, Ap
Sequence 7752, Ap
Sequence 7752, Ap
Sequence 210, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 12270, A
                                                                                                                                                                   (without alignments)
2011.188 Million cell updates/sec
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                                                                                                                                                                                                                                              154
l cggccggagctggtcatctc......gagatgaccagctccggccg
                                                                                                                                         November 19, 2002, 04:53:30 ; Search time 29 Seconds
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/cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubna/USO8_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-906-209-17

US-09-712-363-100

US-09-712-363-100

US-09-812-830A-20

US-09-815-242-7752

US-09-815-242-7752

US-09-815-242-7752

US-09-815-242-7752

US-09-815-242-7752

US-09-860-846-40

US-09-860-846-40

US-09-860-846-40

US-09-861-289-40

US-09-861-289-40
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                                                                                                                                                                                                                                                                                                                                                                        335578 seqs, 189365133 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
                                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                            US-09-887-194A-13
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Query
Match Length DB
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Gaps

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RESULT 2 US-09-906-209-17/c

US-09-815-242-4092

US-09-712-363-81

332.8 331.8 331.6 330.8 330.8 330.8 330.8 330.6 330.6 330.6 330.6 330.6 330.6 330.6

Score

2

Result

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APPLICANT: Elsenbergy David
APPLICANT: Elsenbergy David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: PCT/0800/02246
PRIOR PILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/17/844
PRIOR APPLICATION NUMBER: 60/17/844
PRIOR PILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR PLILING DATE: 1999-02-01
PRIOR PLILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR PLILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR PRILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR PILING DATE: 1999-11-12
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                                                                                                             Length 9210;
                                                                                                             Ouery Match 21.3%; Score 32.8; DB 9; Length 92:
Best Local Similarity 59.8%; Pred. No. 1.1;
Matches 55; Conservative 0; Mismatches 37; Indels
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Pred. No. 1.1;
0; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GACGATGAGCGAGATGACCAGCTCCGGCCGCC 119
                                                                                                                                                                                                                                                                                                                                    96 GCGAGATGACCAGCTCCGGCCGCCGACTCGAC 127
  ; TYPE: DNA; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-00-712-363-100/c
Sequence 100, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Elsenberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-822-830A-20
S-99-802-830A-30
S-Sequence 20, Application US/09822830A
Patent No. US20020142952A1
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Best Local Similarity 59.8%;
Matches 55; Conservative (
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APPLICANT: Eisenberg, David
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Serrigio H.
APPLICANT: Rotstein, Serrigio H.
APPLICANT: Marcotte, Edward H.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: DETERMINING OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
PRIOR APPLICATION NUMBER: PCT/US/06/02246
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1999-00-01
PRIOR FILING DATE: 1999-00-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 9210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4974 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGCGCCGCCGACTCGACGATGAGCGAGT 4915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 GACCAGCTCCGGCCGCCGACTCGACGAGATGACCAGCTCCGGCCG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                       APPLICANT: Allen, Steve
APPLICANT: Butler, Karla
APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: Ilaq, Lawrence L.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB141 NA
FURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,712
PRIOR PLING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGHI 4974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%; Score 112; DB 9; 1
100.0%; Pred. No. 5.7e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: unsure
; LOCATION: (9951)
; CHER INFORMATION: n - A, C, G, or T
US-09-906-209-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 100, Application US/09712363 Patent No. US20020164588A1
Sequence 17, Application US/09906209
Patent No. US20020165385A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 112; Conservative
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US-09-712-363-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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64 CGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
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; LOCATION: (1).
US-09-815-242-7752
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APPLICANT:
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                                                                 APPLICANT: Fechtel, Kin

APPLICANT: Fechtel, Kin

APPLICANT: Agostino, Michael J.

APPLICANT: Howes, Steven H.

APPLICANT: Gulukota, Kamalakar.

APPLICANT: Graham, James R.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

FILE REFERENCE: GIN 6402

CURRENT FILING DATE: 2001-03-29

FRICK PILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 631

SEQ ID NO 20

LENGTH: 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 CGCCGCGGATCCTTCGCCCCCAGCTCGGGGACACGCAAAACTGCCAGCTGCGGG 182
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Pred. No. 1.7;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-822-830A-20/C
Sequence 20, Application US/09822830A
Patent No. US20020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
APPLICANT: Gonedics Cardon G
APPLICANT: Langer Clark, Hilary
APPLICANT: Clark, Hilary
                     : Genetics Institute, Inc
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Agostino, Michael J.
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ilarity 54.8%;
Conservative
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il Similarity 54.8%;
63; Conservative
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                                      Wong, Gordon G.
Clark, Hilary
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US-09-822-830A-20
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Best Local Similarity
Matches 63; Conserv
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SEQ ID NO 20
LENGTH: 1573
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APPLICANT:
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Best Local
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43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
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APPLICANT: Xu, Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 06/291,078

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-23

PRIOR PLICATION NUMBER: 60/245,578

PRIOR PLICATION NUMBER: 60/245,578

PRIOR PLICATION NUMBER: 60/245,578

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/250,308

PRIOR FILING DATE: 2000-11-27

PRIOR PLICATION NUMBER: 60/250,308

PRIOR PLICATION NUMBER: 60/22016

PRIOR PLICATION NUMBER: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO 7752

LENTH: 2451
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Pred. No. 2;
0; Mismatches 29;
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; Sequence 7752, Application US/09815242
; Patent No. US20020061569Al
                                                                                                                                          Sequence 7752, Application US/09815242 Patent No. US20020061569A1
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                              APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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62.8%;
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 GACCAGCTCCGGCCGCCG 120
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity 62.8%
Matches 49; Conservative
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeqtic Agents Using TITLE OF INVENTION: Sets.

FILE REFERENCE: 689290-76

CURRENT APPLICATION NUMBER: US/60/233,617

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR PELING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-26

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                   Score 31.4; DB 10;
Pred. No. 2.3;
0; Mismatches 76;
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Pred. No. 2.
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 210.
LENGTH: 3202
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Best Local Similarity 64.4'
Matches 47; Conservative
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; ORGANISM: Homo sapiens
US-09-954-456-210
                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-954-456-210
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Matches 47; Conserv
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US-09-954-456-210/c
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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                                TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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Pred. No. 2;
0; Mismatches 29;
                                                                                                      CURRENT PETEING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
PRIOR PLING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: 2451
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR PLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR PELING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
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Patent No. US20020115057A1
GENERAL INPORMATION:
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.5%;
62.8%;
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                                                                                    FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 62.8 Matches 49; Conservative
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US-09-815-242-7752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
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57 CGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
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                                                                                    117 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                              Sequence 40, Application US/09861289
Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.0%;
Best Local Similarity 57.1%;
Matches 56; Conservative
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LENGTH: 2787
JS-09-861-289-40
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APPLICANT: Liu, H.
APPLICANT: DABO, L.
TITLE OF INVENTION: DBA encoding methymycin and pikromycin FILE REPERENCE: 600.438018.
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR PAPLICATION NUMBER: 09/105,537
PRIOR PALICATION NUMBER: 09/105,537
PRIOR PALICATION NUMBER: 09/105,537
PRIOR PALICATION DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 40
LENGTH: 2787
                                                     Sequence 40, Application US/09860846

Patent No. US20020164742a1

GENERAL INCORMATION:

APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Tabo, L.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin

FILE REFERENCE: 600.4380S1

CURRENT APPLICATION NUMBER: 0S/09/860,846

CURRENT FILING DATE: 2001-05-18

PRIOR PLIING DATE: 1998 06-26
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; Sequence 40, Application US/09860846
; Patent No. US20020164742A1
; GENERAL INFORMATION:
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; ORGANISM: Streptomyces venezuelae
US-09-860-846-40
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Best Local Similarity
Matches 56; Conserv
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LENGTH: 2787
                              JS-09-860-846-40
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Indels

42;

Length 2787;

Score 30.8; DB 10; Pred. No. 3.3;

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                                                                                                                   APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Aleo, Y.
TILE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600, 438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
SPRIOR APPLICATION NUMBER: 09/105,537
SPRIOR SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
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US-09-861-289-40/c
; Sequence 40, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces venezuelae
US-09-861-289-40
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Search completed: November 19, 2002, 05:26:35 Job time : 46 secs

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(without alignments)
1103.432 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ar	US-09-887-194A-13	US-09-887-194A-13	US-09-934-900-25	US-09-934-900-25	US-60-213-961-13	US-60-213-961-13	US-09-906-209-17.	US-09-906-209-17	US-09-934-900-26	US-09-934-900-26	US-09-887-194A-29	US-09-887-194A-29	US-09-887-194A-12	US-09-887-194A-12	US-09-934-900-24	US-09-934-900-24	US-60-213-961-12	US-60-213-961-12	US-09-887-194A-14	US-09-887-194A-14	US-60-213-961-14
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& Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	72.7	72.7	53.8	53.8	52.6	52.6	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9
Score	154	154	154	154	154	154	112	112	82.8	82.8	81	81	80	80	80	80	80	80	80	80	80
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Sequence 13, Application US/09887194A
GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F.
APPLICANT: Glassman, Kinherly F.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRES:
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
SUDRENT FILING DATE: 2002-03-13
SOFTWARE: Microsoft Office 97
SED ID NO 15-4
                                                                                                                                                                                                                                                                FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
8 OTHER INFORMATION: region of PKS133
US-09-887-194A-13
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APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9;
TITLE OF INVENTION: ACP Desaturase
FILE REFRENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: MICROSOFT Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 154; DB 35;
100.0%; Pred. No. 6.7e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 154; DB 33; Best Local Similarity 100.0%; Pred. No. 6.7e-25; Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 154; Conservative
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Best Local Similarity
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LENGTH: 154
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GENERAL IMPORMATION:
APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon Kamm, William J.
APPLICANT: Gordon Kamm, William J.
APPLICANT: Groof Con Kamm, William J.
APPLICANT: Minney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 154
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81901, A
25325, A
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30118, A
30118, A
390937,
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                                                             US-60-082-302-335
US-09-815-264-4004
US-09-815-264-4004
US-09-620-392-67826
US-09-702-134-8908
US-09-702-134-8908
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-09-684-016-390937
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-60-197-872-30118
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-09-815-264-81901
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          US-09-887-194A-13/C
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APPLICANT: Gerdon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Steeca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPR FILE REPERENCE: BB1449 US PRV
CURRENT APPLICATION NUMBER: US/60/213,961
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 13
LENGTH: 154
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                                                     ELVISLIVES complementa
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                                    ; FEATURE:
. OTHER INFORMATION: Description of Artificial Sequence:
. OTHER ENTERNATION: region of PKS133
US-60-213-961-13
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100.0%; Pred. No. 6.7e-25;
tive 0; Mismatches 0;
                                                                                                                           DB 65;
                                                                                                                         100.0%; Score 154; DB 65; 100.0%; Pred. No. 6.7e-25;
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                                                                                                                                                                0; Mismatches
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ORGANISM: Artificial Sequence
                 ORGANISM: Artificial Sequence
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Matches 154; Conservative
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Matches 154; Conservative
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APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                           Query Match
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BB1449 US PRV
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                                  CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
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US-09-934-900-25
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Pred. No. 6.7e-25;
; Mismatches 0;
                                                                                                                                                                                                                                                                                    APPLICANT: Caboon, NESDECCA E
APPLICANT: Hitz, William D
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR PILING DATE: 2000-08-22
PRIOR PILING DATE: 2000-08-22
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
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Best Local Similarity 100.0%; Pred. No. 6.7
Matches 154; Conservative 0; Mismatches
                                                                                                          ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Stecce, Kevin L.
APPLICANT: Stecce, Kevin L.
APPLICANT: B1649 US PRV
CURRENT APPLICATION NUMBER: US/60/213,961
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 17
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; GENERAL INFORMATION:
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SEQ ID NO 13
                                                                                                                                                                                                                                                                            APPLICANT: Booth, Russ
                                                                                                                                                                                                  RESULT 4
US-09-934-900-25/c
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APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hitz, William D
APPLICANT: Hitz, William D
APPLICANT: Hitz, William D
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: Bal476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR PPLICATION NUMBER: 60/226996
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: MICROSOft Office 97
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APPLICANT: Galbon, Rebecca E
APPLICANT: Galbon, Rebecca E
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Kinney, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea:
TITLE OF INVENTION: NUMBER: US/09/0934,900
CURRENT APPLICATION NUMBER: US/09/0934,900
CURRENT FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
ORIGINATION FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
SOFTWARE: MICROSOFT Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82.8; DB 35
Pred. No. 3.8e-09;
0; Mismatches 2
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; OTHER INFORMATION: n - A, C, G, OI
US-09-934-900-26
      Sequence 26, Application US/09934900 GENERAL INFORMATION:
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; Sequence 26, Application US/09934900
; GENERAL INFORMATION:
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Best Local Similarity 97.7%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Plasmid pBS68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmid pBS68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Unsure
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                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Micro
SEQ ID NO 26
LENGTH: 6611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEO ID NO 26
LENGTH: 6611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GGAGCTGGTCATCTCGCTCATCGTCGGCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGCCGGAGCTGGTCATCTCGTCGAGTCGGCGGCGGCGGAGCTGGTCATCTCGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4923 CATGTGAGTGGGGGGGGGGCGACTCGACGATGAGCGAGATGACCAGCTCC 4974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CATCGTCGAGTCGGCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.7%; Score 112; DB 34; Length 4974; 100.0%; Pred. No. 1.2e-15; Live 0; Mismatches 0; Indels 0.
## APPLICANT: Ilag, Lawrence L.
| TILE OF INVENTION: Plastidic Phosphoglucomutase Genes FILE REPERENCE: BB1451 NA
| CURRENT APPLICATION NUMBER: US/09/906,209
| CURRENT FILING DATE: 2001-07-16
| PRIOR APPLICATION NUMBER: 60/218,712
| PRIOR FILING DATE: JULY 17, 2000
| NUMBER OF SEQ ID NOS: 17
| SEQ ID NO 17
| SEQ ID NO 17
| LENGTH: 4974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Allen, Steve
APPLICANT: Buller, Karla
APPLICANT: Buller, Karla
APPLICANT: Garlson, Tom
TILE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
FRIOR PELING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
SEQ ID NO 17
LENGTH: 4974
                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (3951)
OTHER INFORMATION: n = A, C, G, Or T
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                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100. Matches 112; Conservative
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Best Local Similarity 100.
Matches 112; Conservative
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US-09-934-900-26

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US-U9-887-194A-12/C

Sequence 12, Application US/09807194A

Sequence 12, Application US/09807194A

GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Reith S.
APPLICANT: Lowe, Reith S.
APPLICANT: Secca, Revin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESTILE REPRENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CUBRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: MICTOSOFT Office 97
SEQ ID NO 12
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
F
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Glassman, Kimberly F.
APPLICANT: Glassman, William J.
APPLICANT: Glassman, William J.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott Office 97
SEQ ID NO 12
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa OTHER INFORMATION: region of PKS106 and PKS124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVISLIVES complementa
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                38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGGTCGCCGCCGCCGACTCGACGATGAGC 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%; Score 80; DB 33; Length 80 (larity 100.0%; Pred. No. 2.3e-08; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS106 and pKS124 US-09-887-194A-12
                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09887194A GENERAL INFORMATION:
                                                                                                                                                                                    903 CATCGTCGAGTCGGCGCCGC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                   61 CATCGTCGAGTCGGCGGCCGC 81
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Matches 80; Conserva
                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-887-194A-12
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APPLICANT: Gordon-Ramm, William J.
APPLICANT: Gordon-Ramm, William J.
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION FILE REFERENCE: BB1449 US NA
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
Sequence 29, Application US/09887194A
GENERAL INFORMATION:
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Keith S.
APPLICANT: Lowe, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION FILE REFERENCE: BB1449 US NA
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: MICROSOft Office 97
SEQ ID NO 29
LENGTH: 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary; OTHER INFORMATION: region of pKS149
US-09-887-194A-29
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5433 ACTCAGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 5374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6%; Score 81; DB 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-08
Matches 81; Conservative 0; Mismatches 0
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                                                                                        5373 ATGAGGGAGATGACCAGCTCCGGCCG 5348
                                                              129 ATGAGCGAGATGACCAGCTCCGGCCG:154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09887194A GENERAL INFORMATION:
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Matches 81; Conservative
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Sequence 24, Application US/09934900

GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Cahoon, Rebecca E
APPLICANT: Milliam D
APPLICANT: Kinney, Anthony
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl:
TITLE OF INVENTION: ACP Desaturase
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NO Desaturase
FILE REFERENCE: BB1476 US NO DESATURATE
CURRENT APPLICATION NUMBER: 05/09/934,900
CURRENT APPLICATION NUMBER: 60/22696
PRIOR PPLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 24

LEATH: 80

LEATH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary:
OTHER INFORMATION: region of pKS106 and pKS124
US-09-934-900-24
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                                                                                   0; Gaps
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    Length 80;
                                               0; Indels
ch 51.9%; Score 80; DB 33; 1
1 Similarity 100.0%; Pred. No. 2.3e-08;
80; Conservative 0; Mismatches 0;
                                                                                                                                                                      98 GAGATGACCAGCTCCGGCCG 117
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                                                                                                                                                                                              20 GAGAFGACCAGCTCCGGCCG 1
  Ouery Match
Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                               RESULT 15
US-09-934-900-24
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1 cggccggagctggtcatctc......gagatgaccagctccggccg 154
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2: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/USO7_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                           224397 seqs, 93841606 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	\$200 3.8 3.3 3.3 3.0 6 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2	Motory Matery 22 6 6 2 2 2 2 6 6 2 2 2 2 6 6 2 2 2 2	Length DB 1681 6 1681 6 1681 6 1681 6 1681 6 1707 6 1707 6 1707 6 1707 6 1707 6 1707 6 11220 6	11000000000000000000000000000000000000	US-10-271-889-7 US-10-271-889-7 US-10-271-889-7 US-09-513-9990-8640 US-09-513-9990-8640 US-10-267-255-68 US-10-267-255-68 US-10-277-889-40 US-10-277-889-40 US-10-277-889-40 US-10-277-889-40 US-10-277-889-40 US-10-277-889-48	00 7 7 7 8 8647 8647 8647 8647 8647 8647 86	· ·
23 24 25 26	27.2 27.2 27.2 27.2	17.8 17.7 17.7 17.7	2327 658 658 795	9999	PCT-USO2-33723-66 US-10-209-582-181 US-10-209-582-181 US-10-267-255-57 US-10-267-255-57	Sequence 66, Appl Sequence 181, App Sequence 181, App Sequence 57, Appl Sequence 57, Appl	

RESULT 2
US-10-271-889-7/C
SCHOOL 7, Application US/10271889
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.

Sequence 29, Appl Sequence 29, Appl Sequence 96, Appl Sequence 11379, A Sequence 11379, A Sequence 1014, Ap Sequence 20, Appl Sequence 34, Appl Sequence 34, Appl Sequence 202, Appl Sequence 202, Appl Sequence 202, Appl Sequence 6, Appl Sequence 6, Appl Sequence 1548, Apsl Sequence 1548, Apsl Sequence 1548, Apsl Sequence 1548, Appl Sequence 1548	ii.	Length 1681; Indels 0; Gaps 0; AGCTGGTCATCTCGCT 60
US-10-267-255-29 US-10-267-255-29 US-10-267-255-96 US-10-267-255-96 US-10-267-255-96 US-10-213-999C-13979 US-10-240-425-1014 US-10-240-425-1014 US-10-257-022-20 US-10-257-022-20 US-10-257-022-20 US-10-257-022-20 US-10-271-889-34 US-10-271-889-34 US-10-271-889-34 US-10-271-889-34 US-10-271-889-34 US-10-271-889-34 US-10-271-889-34 US-10-285-876-6 US-10-285-876-6 US-10-240-425-1548 US-10-240-425-1548 US-10-240-425-1548	ALIGNMENTS 271889 ding Methymycin and Pikromycin US/10/271,889 0-15 09/861,289 8 8 8 8 09/860,846 7 09/105,537 6 8 Version 4.0	e 34.8; DB 6; . No. 0.26; 1smatches 52; TCGAGTCGGGGCGG
4 4 813 6 813 6 813 6 813 6 813 8 8 813 8 8 813 8 8 8 8 8 8 8 8 8 8	/10 18: 2-1 2-1 2-1 0 S 1 S 1 S 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C	Streptomyces narbonensis 7 22.6%; Scor imilarity 55.9%; Pred ; Conservative 0; M GGGGGTGGTCATCGCTCATCG
26.8 26.8 26.8 26.8 26.6 17. 26. 26.6 17. 26. 26.6 17. 26.7 17. 26.7 17. 26.7 17. 17. 17. 17. 17. 17. 17. 17. 17. 1	RESULT 1 US-10-271-889-7 Sequence 7, Application US GENERAL INFORMATION: APPLICANT: Sherman, D.H.: APPLICANT: Liu, H. APPLICANT: D.H. FILE REFERENCE: 600.582US CURRENT PAPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR PLILING DATE: 2001-0 PRIOR FILING DATE: 1998-0 NUMBER OF SEQ ID NOS: 55 SOFTWARRE: FASTESD for Winn	
	RESULT 1 US-10-271-(Sequence) GENERAL APPLICAL AP	; TENGIN ; TENGIN ; ORGANI US-10-271- Query Me Best Loc Matches Oy 1 Db 424 Oy 61

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% Sequence 8640, Application US/09513999C

| Sequence 8640, Application US/09513999C
| GENERAL INFORMATION:
| APPLICANT: Dunclert, A. |
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| TITLE OF INVENTION: DATE: 2000-02-24 |
| PRIOR FILING DATE: 2000-02-24 |
| PRIOR FILING DATE: 1999-02-26 |
| NUMBER OF SEQ ID NOS: 36681 |
| SOSTWARE: Patent.pm
                                                                                                                                                         Gaps
                                                                                                                                                                                                                      246 GCCGGACGTGGTGATTCTCTCACCACCCACCTACGCCCGACGTGGTCCTTTCCCTCA 305
                                                                                                                                                                                                  3 GCCGGAGCTGGTCATCTCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCA 62
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Pred. No. 0.58;
2; Mismatches 27; Indels
                                                                                                             Length 345;
                                                                                                                                                       27; Indels
                                                                                                             Score 33; DB 5;
Pred. No. 0.58;
2; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.4%;
Best Local Similarity 62.3%;
Matches 48; Conservative 3
                                                                                                               Query Match 21.4%;
Best Local Similarity 62.3%;
Matches 48; Conservative
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US-09-513-999C-8640
                                                                                                                                                                                                                                                                                                             306 CCACCCAGCCTACYKYC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 AGATGACCAGCTCCGGC 152
                                                                                                                                                                                                                                                                                      63 regregaereseese 79
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        ; NAME/KEY: misc_feature
; LOCATION: 345
; OTHER INFORMATION: m-a or
US-09-513-999C-8640
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FEATURE:
NAME/KE:
LOCATION: 319
OTHER INFORMATION: y-c or
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: 73
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LENGTH: 345
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 8640
LENGTH: 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.6%; Score 34.8; DB 6; Length 1681; Best Local Similarity 55.9%; Pred. No. 0.26; Matches 66; Conservative 0; Mismatches 52; Indels 0
TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin FILE REFERENCE: 600.582081
CURRENT APPLICATION NUMBER: US/10/271.889
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/861,289
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 1908-06-26
NUMBER OF SCO ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-10-271-889-7
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OTHER INFORMATION: y-c or t
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OTHER INFORMATION: k-g or t
FEATURE:
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MAME/KEY:
LOCATION: 73
OTHER INFORMATION: n=a, g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 319
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NAME/KEY: misc_feature
.....TON: 320
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NAME/KEY: misc_feature
LOCATION: 321
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LOCATION: 336
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-513-999C-8640
                                                                                                                                                                                                                                                                                                                                 LENGTH: 1681
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Gaps

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Db 46289 GCGGTTCTTCATGTGCATGATCCAGAACCCGGGGTTCGACGGGGCGGTGATGAGCTCAA 46348
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                                                                                                                                                                                                                                                    5 CGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGGTCATCTCGCTCATC 64
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                                     20.4%; Score 31.4; DB 6; Length 1707; 56.2%; Pred. No. 2.1; ive 0; Mismatches 46; Indels 0
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APPLICANT: He, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REPRENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46349 CACCCGGGCCGCTGCTGCGCGCGGTGGACTACGACCGGCCCG 46393
                                                                                                                                                                                                                                                                                                                                                                                                                     710 GCCCCGTCGAACCCCGGGTTCTGGATCATGCACATGAAGAACCGC 666
                                                                                                                                                                                                                                                                                                                                                                65 GTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGC 109
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FILE REFERENCE: 600.4560831
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 2002-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR FILING DATE: 1999-03-12
PRIOR PELING DATE: 1990-03-12
PRIOR PELING DATE: 1996-08-19
PRIOR FILING DATE: 1996-08-19
PRIOR PILING DATE: 1994-10-06
PRIOR PILING DATE: 1994-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSEQ for Windows Version 3.0
SERIOR PILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSEQ for Windows Version 3.0
SERIOR NOT 500 DATE: 1990-10-07
LENGTH: 53500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 76, Application US/10267255 GENERAL INFORMATION:
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; ORGANISM: Streptomyces lavendulae
US-10-267-255-76
                                                                                  al Similarity 56.2
59; Conservative
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                                         Query Match
Best Local S
Matches 59
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APPLICANT: Various M.

APPLICANT: He, M.

APPLICANT: Sheldon, M.

TITLE OF INVENTION: Mitomycin biosynthetic gene cluster.

FILE REFERENCE: 600.456081

CURRENT PEPLICATION NUMBER: US/10/267,255

CURRENT FILING DATE: 1099-03-12

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1996-08-19

PRIOR FILING DATE: 1994-10-06

PRIOR FILING DATE: 1994-10-06

PRIOR FILING DATE: 1994-10-06

PRIOR FILING DATE: 1994-10-06

PRIOR FILING DATE: 1993-10-07

NUMBER OF SEQ ID NOS: 145

SOFTWARE: FASISEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Macy I. Macy I. Mach I. Mac
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: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-10-267-255-68
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US-10-267-255-68
262 AAATGACCACGTCGGGC 246
                                                                                                                                                                                                                                                                             APPLICANT: Sherman, D
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LENGTH: 1707
                                                                                                                                                     US-10-267-255-68
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Score 30.8; DB 6; Length 2787;
Pred. No. 3.3;
0; Mismatches 42; Indels 0
     APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
FILE REPERENCE: 600.582013
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR PLICATION NUMBER: US 09/860,846
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CATCGTCGAGTCGGCGGCGCCGACTCGACGATGAGCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Genbank Accession No. X02344
US-10-240-425-1526
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Best Local Similarity 54.9%; Pred. No. 15;
Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces venezuelae
US-10-271-889-40
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Best Local Similarity 57.1%;
Matches 56; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 40
LENGIH: 2787
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                     DB 6; Length 53500;
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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin FILE REFERENCE: 600-582031
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT APPLICATION NUMBER: US 09/861,289
PRIOR FILING DATE: 2001-05-18
PRIOR PELING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/860,846
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/336,821
PRIOR APPLICATION NUMBER: US 09/336,821
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 2787
                                                                                                                                                                                                                                                                                                Ouery Match 20.4%; Score 31.4; DB 6; Length 5
Best Local Similarity 56.2%; Pred. No. 3.9;
Matches 59; Conservative 0; Mismatches 46; Indels
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PRIOR APPLICATION NUMBER: PCT/US94/11279
PRIOR FILLING DATE: 1994-10-06
PRIOR APPLICATION NUMBER: US 08/133,963
PRIOR FILLING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 76
LENGTH: 53500
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; GENERAL INFORMATION:
                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-10-267-255-76
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GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Watzel, Uwe
APPLICANT: Wetzel, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Wetzel, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44021-50.26
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
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US-10-271-889-32/c
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  Query Match
Best Local Si
Matches 62;
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                                                                                                                                                                  APPLICANT: LOTG, MUND APPLICANT: APPLICANT: APPLICANT: AIVATEZ, Chris APPLICANT: ALVATEZ, Chris APPLICANT: Wetzel, Jon C.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Wockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2001-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ 1D NOS: 1588
SOFTWARE: PatentIN Ver. 2.1
SEQ 1D NO 1526
LENGTH: 3284
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APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin FILE REFERENCE: 600.582US1
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/860,846
PRIOR APPLICATION NUMBER: US 09/860,846
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 1999-06-26
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Pred. No. 15;
0; Mismatches 46; Indels
717 CCTCTTCCCCGCCGCCGCCGCCGCCATCATGAGGGAAAT 758
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CHER INFORMATION: Genbank Accession No. X02344
US-10-240-425-1526
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                       Sequence 1526, Application US/10240425 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%;
                                                                                                                                              APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
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Best Local Similarity 54.99
Matches 56; Conservative
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                                                                RESULT 12
US-10-240-425-1526/c
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US-10-271-889-32
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                                                                                                                                                                                                                                                                                 Db 10620 CCAGCGCAGGGCAGCCCCGGAGGCGCGGGCGAGGCGGACACGGACCTCGGCGGGGGG 10677
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DB 6; Length 11220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sherman, D. H.
APPLICANT: Sherman, D. H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin FILE OF INVENTION: DNA Encoding Methymycin and Pikromycin FILE OF INVENTION: DNA Encoding Methymycin and Pikromycin FILE OF INVENTION: DOS 100-10-15
CURRENT APPLICATION NUMBER: US 09/861, 289
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/816, 821
PRIOR APPLICATION NUMBER: US 09/816, 821
PRIOR APPLICATION NUMBER: US 09/816, 821
PRIOR APPLICATION NUMBER: US 09/105, 537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SED ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Xue, Y.
APPLICANT: ADO, I.
TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin CURRENT ENGO SABJUSI.
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT FILING DATE: 2002-10-15
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52.5%; Pred. No. 18;
Live 0; Mismatches
  Score 28.4; 1
Pred. No. 18;
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PRIOR FILING DATE: 2001-05-18
PRIOR PAPLICATION NUMBER: US 09/860, 846
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/836, 821
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APPLICATION NUMBER: US 09/105,537
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/10271889 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Streptomyceş venezuelae
US-10-271-889-32
18.4%;
ilarity 52.5%;
Conservative (
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                          1 Similarity
62; Conserv
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Search completed: November 19, 2002, 05:29:53 Job time: 194 secs

Title: Perfect score: Sequence:

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Run on:

Scoring table:

Searched:

Database

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AL263194 Tetracdon
AL265194 Tetracdon
AL306535 Tetracdon
BQ767987 EBro08_SQ
AL399069 NCWOLBLIT
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BF483067 WHE2314_D
BQ805125 WHE3563_B
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BQ841269 WHE4209_A
AL238754 Tetracdon
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                      CNSO3W2P
CNSO4TDK
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BQ767987
A1399069
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BG805125
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                                                                      November 19, 2002, 05:26:44 ; Search time 2117 Seconds (without alignments) 1178.132 Million cell updates/sec
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154
1 cggccggagctggtcatctc......gagatgaccagctccggccg 154
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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BI960178 HVSMEn002 BI960178 HVSMEn002 AU078265 AU078265

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_other:* em_gss_pro:* em_gss_rod:*

em_gss_mus:*

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			Description	DD045040 CM0_NN115	CTINNIONO KECC	5949 CM0-NN115	3156 Tetraodon	3156 Tetraodon	A2933792 BJ Ba000	2933792 BJ Ba000	
			escr	7000	7	BF94	AL25	AL25	A293	A293	
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RESULT 1 BF945949	
rocus	BF945949 175 bp mRNA linear EST 22-JAN-2001
DEFINITION	55-271000-628-a09 NN1155 Homo sapiens CDNA,
ACCESSION	
VERSION	BF945949.1 GI:12363224
KEYWORDS	EST.
SOURCE	human .
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 175)
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
	Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
	Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
	Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
	, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
	Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed
	sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.
	Laboratory of Cancer Genetics
	Ludwig Institute for Cancer Research
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
	D1451-11-2704022
	741.1 - 7.5 1 1 - 7.0 1 1
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High quality
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JOURNAL
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                           FEATURES
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                                                                                                                                                                                                                                                                                                    /note="Organ: nervous_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Silmson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                  This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-NNI155-271000-628-a09&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence start: 13
High quality sequence stop: 175.
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This sequence was derived from the FAPESP/LICK Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti-CMOst2=CMO-NNI155-
271000-6528-a09543-2000-10-274t4-1)
Seq primer: puc 18 forward
High quality sequence start: 13
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36.6; DE
Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1155"
/dev_stage="Adult"
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 TGAGCGAGATGACCAGCTCCGGC 152
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Matches 54; Conservative
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSO30BV 627 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 041B18 of library G from Tetraodon nigroviridis, genomic survey
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
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cost-Crollius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 GCCGGACGTGGTCATTTCTCTCACCACCCAGCCTACCGCCCGACGTGGTCCTTTCCCTCA 30
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 175;
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/db xref="taxon:99883"
/clone="041B18"
/clone_lib="G"
                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.6; |
Pred. No. 36;
ity sequence stop: 175.
Location/Qualifiers
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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us-09-887-194a-13.rst

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Bradyrhizobium japonicum.
Bradyrhizobium japonicum
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Bradyrhizobium japonicum
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Class: BAC ends
                                                                                                                                                                                                                                                         AZ933792.1 GI:13775852
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                    354 GACCATGAGCGAG 342
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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1 (bases 1 to 627)

2 (bases 1 to 627)

2 (bases 1 to 627)

2 (bases 1 to 627)

3 (bases 1 to 627)

3 (bases 1 to 627)

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9 (bases 1 to 627)
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
            : COBGO41DA09LP1-end : T7"
5 others
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5 others
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/db_xxef="taxon:99883"
/clone="041818"
                                                                                                        Score 36.2; DB 17;
Pred. No. 54;
0; Mismatches · 28;
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/note="Genoscope sec
168 c 210 g
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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/note="Genoscope :
168 c 210
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                                                                                                      23.5%;
65.4%;
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68.5%;
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Matches 53: Conserv
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BJ_Ba0001E22f B. japonicum BAC library Bradyrhizobium japonicum pactumic, DNA sequence.
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Bradyrhizobiaceae; Bradyrhizobium.
1 (bases I to 78).
Tomkins, J.P., Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A., Goicoechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                         GSS 24-APR-2001
                                                                                                                                                                                                                                                                                                                                                         Loh, J.T., Judd, A., Goicoechea
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                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 787)

Tomkins, J.P., Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A., Goicoechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
787 bp DNA linear GSS 24-APR-20

BJ__Ba0001E22f B. japonicum BAC library Bradyrhizobium japonicum

A2933792
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Bradyrhizobiaceae; Bradyrhizobium.
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241 c 267 g 167 t l others
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/strain="USDA110"
/db_wrie="Laxon:375"
/clone_lib="B. japonicum BAC library"
/lab_host="E. col1"
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60.8%; Pred. No. 56;
tive 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
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1 (bases 1 to 1057)

1 (bases 1 to 1057)

Bernot, A., Fizames, C., Mincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using meanist.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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/lab_host="E. coli"
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/strain="USDA110"
/db_xref="taxon:375"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwingeclemson.edu
Class: BAC ends
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High quality sequence stop: 732.
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Submitted (12-APR-2000)
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hes 59; Conservative
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CUNSUSWER 1057 bp DNA Thear GSS 18-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 063118 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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[ (base; to 1057)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Pisher, C., Bernot, A., Pizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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                                                             | 1.1057 | /organism="Tetraodon nigroviridis" | //db_xrof="texton:99883" | /clone="063118" | /clone="1ib="6" | /clone="16" | /clone="6enoscope sequence ID : COBGG | /note="Genoscope sequence ID : COBGG | /note="5enoscope sequence ID : COBGG | /note | /note="5enoscope sequence ID : COBGG | /note | /note="5enoscope sequence ID : COBGG | /note 
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Location/Qualifiers
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Best Local Similarity

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REFERENCE AUTHORS

RESULT 9 CNS04TDK

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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
      CNSO4TDK 972 bp DNA linear GSS 24-MAY-2000 Tetraodon nigroviridis genome survey sequence T3 end of clone 013112 of library A from Tetraodon nigroviridis, genomic survey
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EBro08_SQ010_K07_R root, 3 week, drought-stressed, cv Optic, EBro08

Hordeum vulgare cDNA clone EBro08_SQ010_K07 5', mRNA sequence.
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1 (bases 1 to 972)  
2 (bases 1 to 972)  
3 (bases 1 to 972)  
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCG 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="013112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 17;
Pred. No. 64;
0; Mismatches 38
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                                                                                                                                                            AL306353.1 GI:8204690
GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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254 c 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000)
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BQ767987.1 GI:21976461
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Best Local Similarity 60.0%;
Matches 57; Conservative
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Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                        CNSW4TDK 972 bp DNA linear GSS 24-MAY-2000 Tetracdon nigroviridis genome survey sequence T3 end of clone 013112 of library A from Tetracdon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Terraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodontidae; retraodon.
1 (bases 1 to 972)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 972)
Cost.Collius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 64; .
0; Mismatches 38; Indels
   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="013112"
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    972 bp
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AL306353.1 GI:8204690
GSS; genome survey sequence.
Tetraodon nigroviridis.
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Conservative
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Matches 57; Conservative
                                                                                                                                                                                   GACGATGAGCGAG 100
                                                                                                                                                                                                                                              510 GACCATGAGCGAG 498
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CNSO4TDK/c
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REFERENCE AUTHORS

JOURNAL

TITLE

TITLE JOURNAL COMMENT

FEATURES

JOURNAL REFERENCE AUTHORS

TITLE

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Gaps

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/note="Vector: psPoRTI; Site_1: Sal 1; Site_2: Not I; 
Non-normalised library, directionally cloned into psPoRTI. 
Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEBRAD funded cereal IGF (Investigating Gene Function) project. 
1 15 37 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa
Eukaryota: Fungi; Ascomycota: Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
I (bases 1 to 590)
Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyee,E.,
Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R.,
Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R.,
Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI399069 · 590 bp mRNA linear EST 08-FEB-1999 NCW01B11T3 Westergaards Neurospora crassa cDNA clone W01B11 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,D.O. Expressed seguences from conidial, mycelial, and sexual stages of
                           /cuitivar="Optic"
/db_xref="taxon:4513"
/clone="EBE008_S0010_K07"
/clone=lib="root, 3 week, drought-stressed, cv Optic,
EBE008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 GTCGAGTCGGCGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGCCGACTC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                      DB 14; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
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/strain="74-0R23-IV A (FGSC 2489)"
/db.xref="taxon:5141"
/clone="WOlBli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Natvig,D.O./Nelson,M.A.
Department of Balology
Oliversity of New Mexico
Castetter Hall, Albuquerque, NM 87131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.8; DI
Pred. No. 62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Westergaards"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                       /dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                    /tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ngp@biology.unm.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI399069.1 GI:4242154
                                                                                                                                                                                                                                                                                                                                                                                                      23.2%;
55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 55.1
Matches 70; Conservative
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Fax: 505 277 0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 GCTGCCG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 CCGGCCG 154
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BQ767987.1 G1:21976461
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Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Triticeae; Hordeum.

1 (bases 1 to 367)

Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,

Development of Barley Transcriptome Resources

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-vector: pSPORT1; Site_1: Sal 1; Site_2: Not 1; Nor normalised library, directionally cloned into pSPORT1. Non-normalised library, directionally cloned into pSPORT1. plants. Developed as part of the harley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
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/db_aref="EBro08_SQ010_K07"
/clone_lib="root, 3 week, drought-stressed, cv Optic,
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Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
Contact: Waugh R. Marshall DF Genome Dynamics/Computational Biology Scottish Crop Research Institute Invergowile, Dundee, DD2 5DA, Scotland, UK Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: eceteeri.sari.ac.uk.
Location/Qualifiers
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Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.2%; Score 35.8; D
55.1%; Pred. No. 62;
ive 0; Mismatches
                                                                                                                                                                                                                                                      /organism-"Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene Function) project.
                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
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Location/Qualifiers
                                                                                                                                                                                                                                                                              /cultivar="Optic"
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Best Local Similarity
Matches 70; Conserv
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1 (Dases 1 to 590)

Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,
Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, E.,
Cushing, T., Errett, A., Fleharty, M., Gorman, Judson, K., Miller, R.,
Ortega, J., Pavlova, I., Perrea, J., Todisco, S., Trujillo, R.,
Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig
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Expressed sequences from conidial, mycelial, and sexual stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.4; DB 9; Length 590;
Pred. No. 82;
0; Mismatches 47; Indels
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/db_xref="taxon:5141"
/clone="W01B11"
/clone="10="Westergaards"
/sex="Mating type A"
/tissue_type a"
/tissu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 CCGCGGTTACCANTACCAGTCTCAGTCAGCCCCAGCCGGACAGTGGCC 190
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University of New Mexico
Castetrer Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ngp@biology.unm.edu.
Location/Qualifiers
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Best Local Similarity 57.3%;
Matches 63; Conservative (
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Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Tritticeae; Tritticeae; Tritticeae; Tritticeae; Tritticeae; Tritticeae; Tritticeae; Tritticeae; Tritticeae; Pooideae; Tobases 1 to 441)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                     BF483067 441 bp mRNA linear EST 06-DEC-2000 WHE2314_D05_G10ZS Wheat pre-anthesis spike cDNA library Triticum aesituum cDNA clone WHE2314_D05_G10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
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                                                                                                                                                                         190 GGCCACTGTCCGGCTGGGGCTGAGTATGAGACTGGTANTGGTAACCGCGGCGGCGGCCCT 131
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                                                                                                              28 GTCGAGTCGCCGGCGGAGCTGGTCATCTCGCTCGATCGTCGCGGCCGCCGCCGACTC 87
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
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Length 590;
                                                                                                                                                                                                                                   88 GACGATGAGCGAGATGACCAGCTCCGGCCGACTCGACGATGAGCGAG 137
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                                                                                                                                                                                                                                                                                       130 GGAGACCAGCGAGGCTGTTGGCGGCGGCTTCTGGGCGATGAGCGAG 81
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Triticum aestivum"
Score 35.4; 1
Pred. No. 82;
                                                          0; Mismatches
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/db_xref="taxon:4565"
/clone="WHE2314_D05_G10"
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23.0%; 57.3%;
                                                          Conservative
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                                 Best Local Similarity
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Search completed: November 19, 2002, 07:49:42 Job time : 2131 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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 OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	November 19, 2002, 05:24:44; Search time 2709 Seconds (without alignments) 1654.423 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-887-194A-13 154 1 cggccggagctggtcatctcgagatgaccagctccggccg 154
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	Minimum DB seg length: 0 Maximum DB seg length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_ln:*
4: gb_ow:*
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6: gb_pa::*
7: gb_ph:*
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11: gb_sts:*
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID 154 100.0 154 6 Ax357128 Ax357128 Sequence 154 100.0 154 6 Ax357128 Ax357128 Sequence 154 100.0 154 6 Ax353724 Ax335724 Sequence 154 100.0 154 6 Ax335724 Ax335724 Sequence 158 100.0 154 6 Ax335724 Ax335724 Sequence 158 100.0 154 6 Ax335724 Ax335724 Sequence 158 100.0 154 6 Ax335724 Ax335724 Sequence 157 4974 6 Ax335724 Ax335724 Sequence 158 15.2 6 6611 6 Ax335724 Ax335724 Sequence 158 15.2 6 6611 6 Ax335724 Ax335724 Sequence 159 80 6 Ax367127 Ax367127 Sequence 150 80 6 Ax367129 Ax367127 Sequence 150 80 6 Ax367129 Ax367127 Sequence 150 80 6 Ax367129 Ax367129 Sequence 150 80 Ax367129 Ax367129 Sequence 150 Ax367129 Ax367129 Sequence 150 Ax367129 Ax367139 Sequence 150 Ax367139 Ax367139 Sequence 150 Ax367139 Ax367139 Sequence 150 Ax367139 Sequence 150 Ax367139 Sequence 150 Ax367139 Sequen	Q Q	Pesult		Out of the				
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ALIGNMENTS

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AX367128 154 bp	Sequence 13 from Patent WO0200904. AX367128	AX367128.1 GI:18855329		synthetic construct artificial sequences.	1	Glassman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L. and Nichols, S.E.	Recombinant constructs and their use in reducing gene expression Patent: WO 0200904-A 13 03-JAN-2002;
RESULT 1 AX367128 LOCUS	DEFINITION	VERSION KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE JOURNAL

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AX392336 154 bp
Sequence 25 from Patent W00216565.
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Recombinant constructs and their use in reducing gene expression
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E. I. du Pont de Nemours and Company (US); PIONEER HI-BRED
INTERNATIONAL, INC. (US)
Location/Qualifiers
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E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
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/db_xref="taxon:32630"
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Nucleotide sequences of a new class of diverged delta-9
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Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
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E. I. du Pont de Nemours and Company (US)
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E. I. du Pont de Nemours and Company (US)
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Pred. No. 8.3e-07;
J; Mismatches 2;
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Sequence 26 from Patent WO0216565.
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Patent: EP 1174510-A 17 23-JAN-2002;
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/db_xref="taxon:32630"
1 1070 c 1003 g 1456 t
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Sequence 17 from Patent EP1174510.
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and Nicholz, S.E.
Recombinant constructs and their use in reducing gene expression
Patent: WO 0200904-A 12 03-JAN-2002;
B. i. du Pont de Memours and Company (US); PIONEER HI-BRED
INTERNATIONAL, INC. (US)
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS106 and
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS106 and
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Recombinant constructs and their use in reducing gene expressatent: WO 0200904-A 12 03-JAN-2002;
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100.0%;
                   61 CATCGTCGAGTCGGCGGCCGC 81
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS149"
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS149"
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1 Similarity 100.0%; Pred. No. 2.5e-06;
81; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                    Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S. Nucleotide sequences of a new class of diverged delta-9 stearoyl-acp desaturase genes stearoyl-acp desaturase genes. Patent: WO 0216565-A 24 28-FEB-2002; E. I. du Pont de Nemours and Company (US)
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/db_xref="taxon:32630"
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pKS124"
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS106 and
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                        CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
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Patent: Wo O21655-A 24 28 FEB-2002;
E. I. du Pont de Nemours and Company (US)
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6e-06;
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Sequence 24 from Patent WO0216565.
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Recombinant constructs and their use in reducing gene expression Patent: WO 0200904-A 14 03-JAN-2002;
E. I. du Pont de Nemours and Company (US); PIONEER HI-BRED
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tive 0; Mismatches 0; Indels
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/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"
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Sequence 14 from Patent WO0200904.
AX367129
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Location/Qualifiers
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Best Local Similarity 100.
Matches 80; Conservative
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